

Ant olfactory receptors underwent dramatic expansion and positive selection



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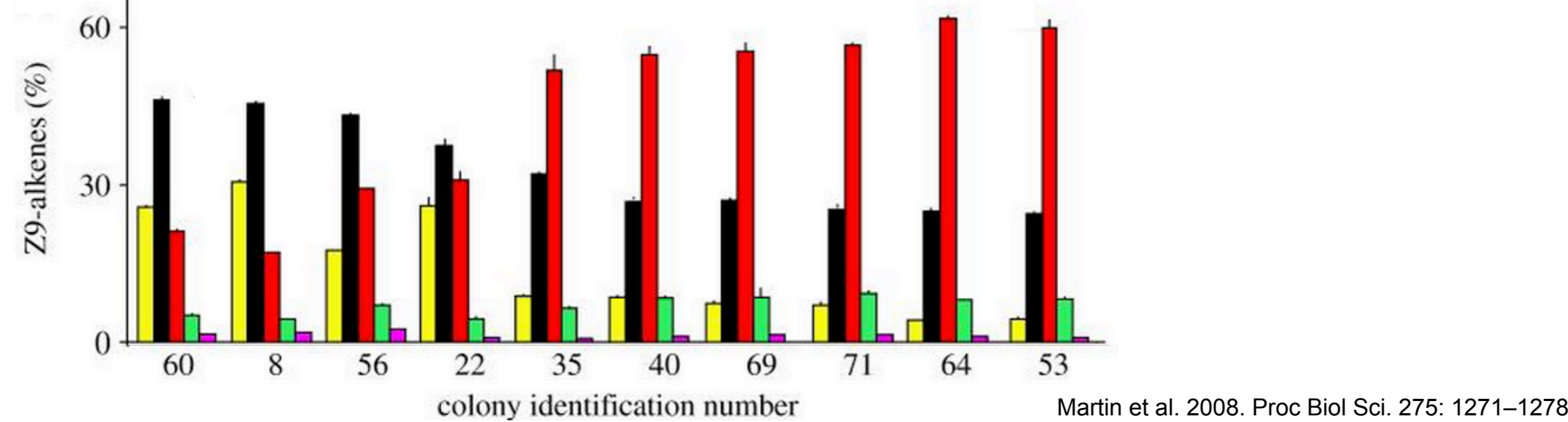
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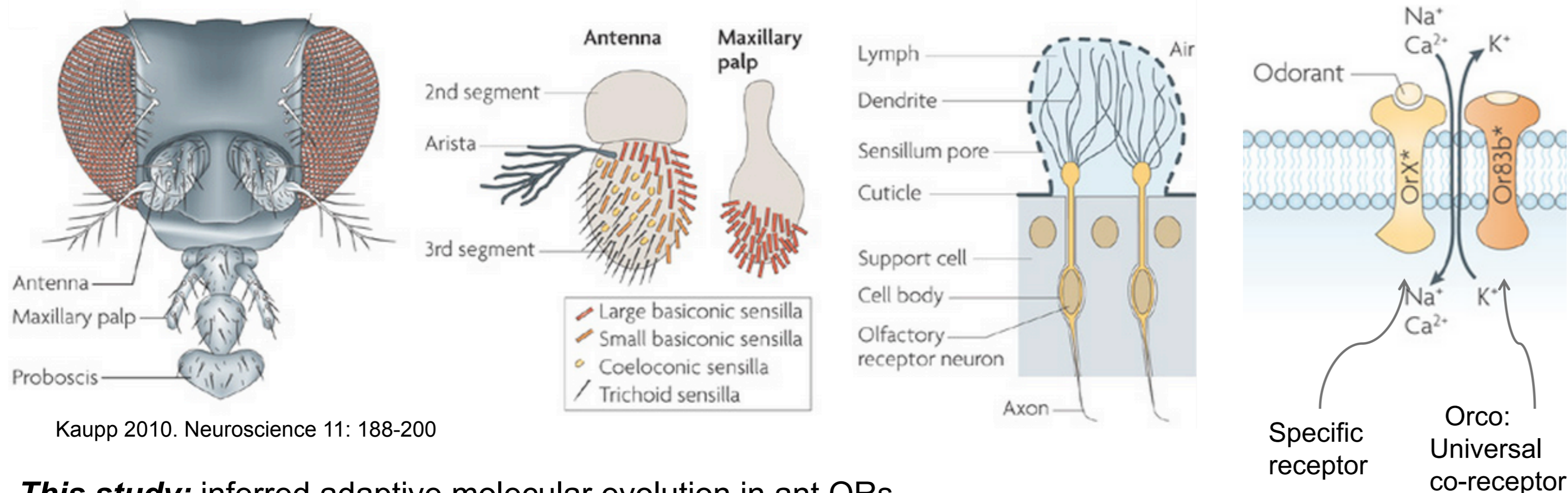


Olfaction is the basis for social communication in ants

Social insects rely mainly on chemical signaling for communication and coordination. A classical example: **nestmate recognition** based on the profile of very long chain cuticular hydrocarbons



Olfactory/odorant receptors (ORs) in insects' antennae and maxillary palp are responsible for recognition of pheromones and other molecules through their specific binding



This study: inferred adaptive molecular evolution in ant ORs

Results: Dramatic expansion (gene duplication) and recurrent positive selection on the amino acid sequence in ant ORs imply extensive adaptation at the molecular level and provides a candidate gene list for further study of the molecular basis of chemical communication

Materials and Methods

Sequences: coding sequences from manually annotated (by Hugh Robertson) OR gene models from two ants and one parasitoid wasp (as outgroup):

262	<i>Nasonia vitripennis</i> (parasitoid wasp)
319	<i>Linepithema humile</i> (ant)
291	<i>Pogonomyrmex barbatus</i> (ant)

Big tree (872 seq):

MAFFT alignment of amino acids (accurate variant E-INS-i)
GUIDANCE reliability masking (permissive cutoff = 0.2)
RAxML tree

Katoh 2008, MBE 9: 286-298
Privman et al. 2012, MBE 29: 1-5
Stamatakis 2006, Bioinformatics 22: 2688-2690

Too big for PAML → split to subtrees in high-bootstrap branches

For each of 16 subtrees (12-99 seq):

PRANK alignment, reverse-translate to a codon alignment
GUIDANCE masking of unreliable codons (stringent cutoff = 0.9)
RAxML tree (based on amino acids)
PAML branch-site test for positive selection (based on codon sequences)
FDR correction

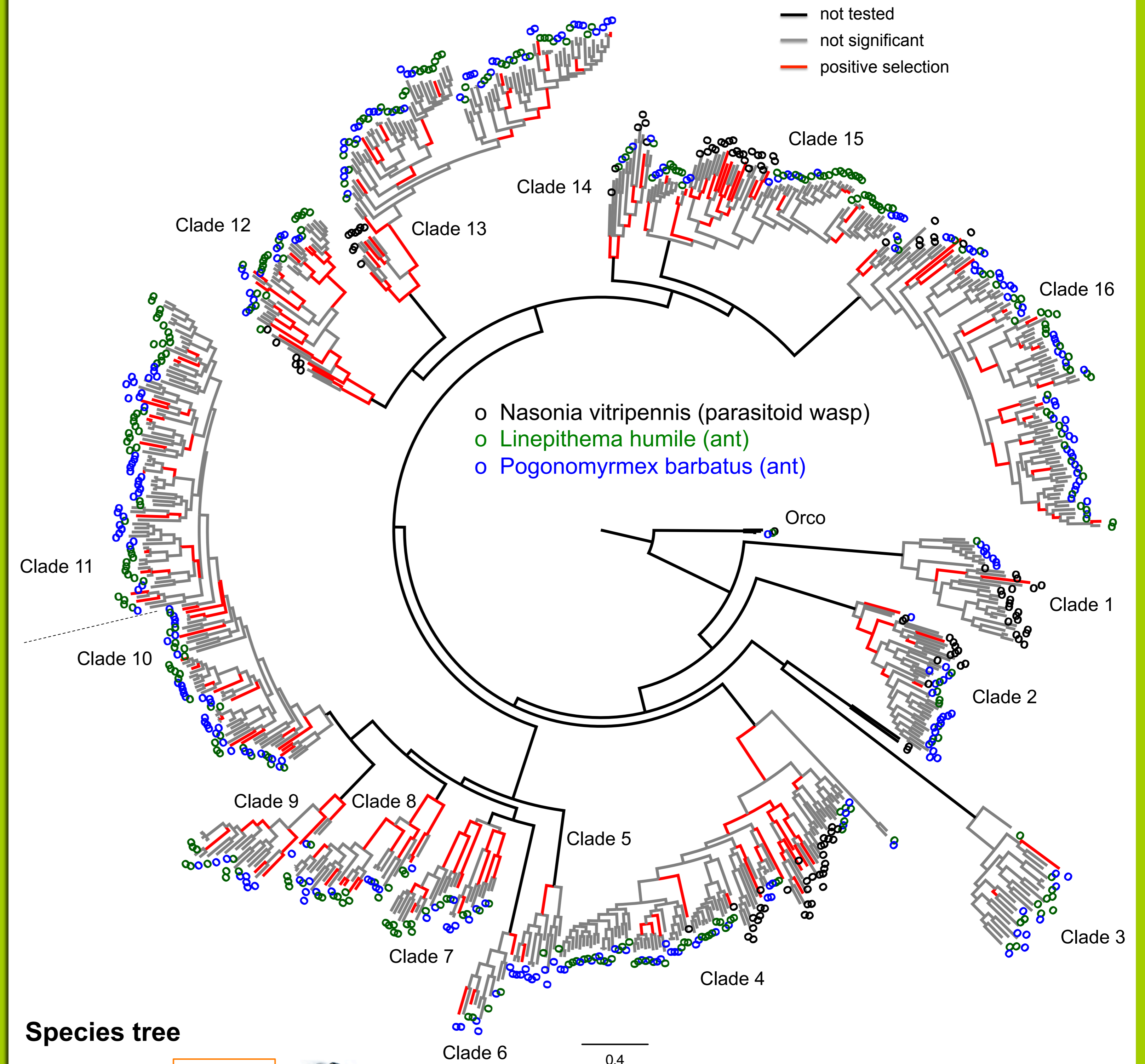
Loytynoja & Goldman 2005, PNAS 102: 10557–10562
Privman et al. 2012, MBE 29: 1-5
Stamatakis 2006, Bioinformatics 22: 2688-2690
Zhang et al. 2005, MBE 22: 2472-2479
Binjamini & Hochberg 1995

OR gene tree: lots of ant-specific duplications

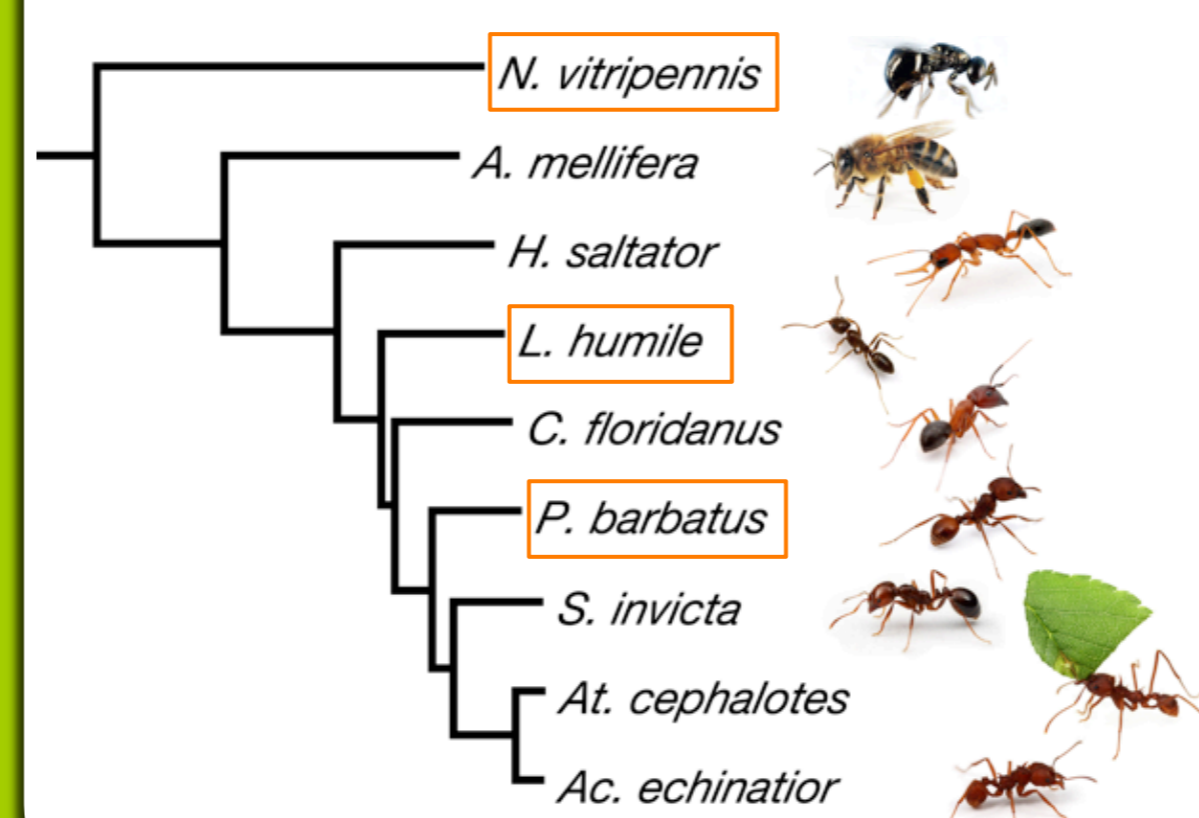
Positive selection inference

using the PAML branch-site (d_N/d_S) test

— not tested
— not significant
— positive selection



Species tree



PhyML phylogeny reconstruction based on 2756 genes by Robert Waterhouse; pictures by Alex Wild.